

FIG. 1

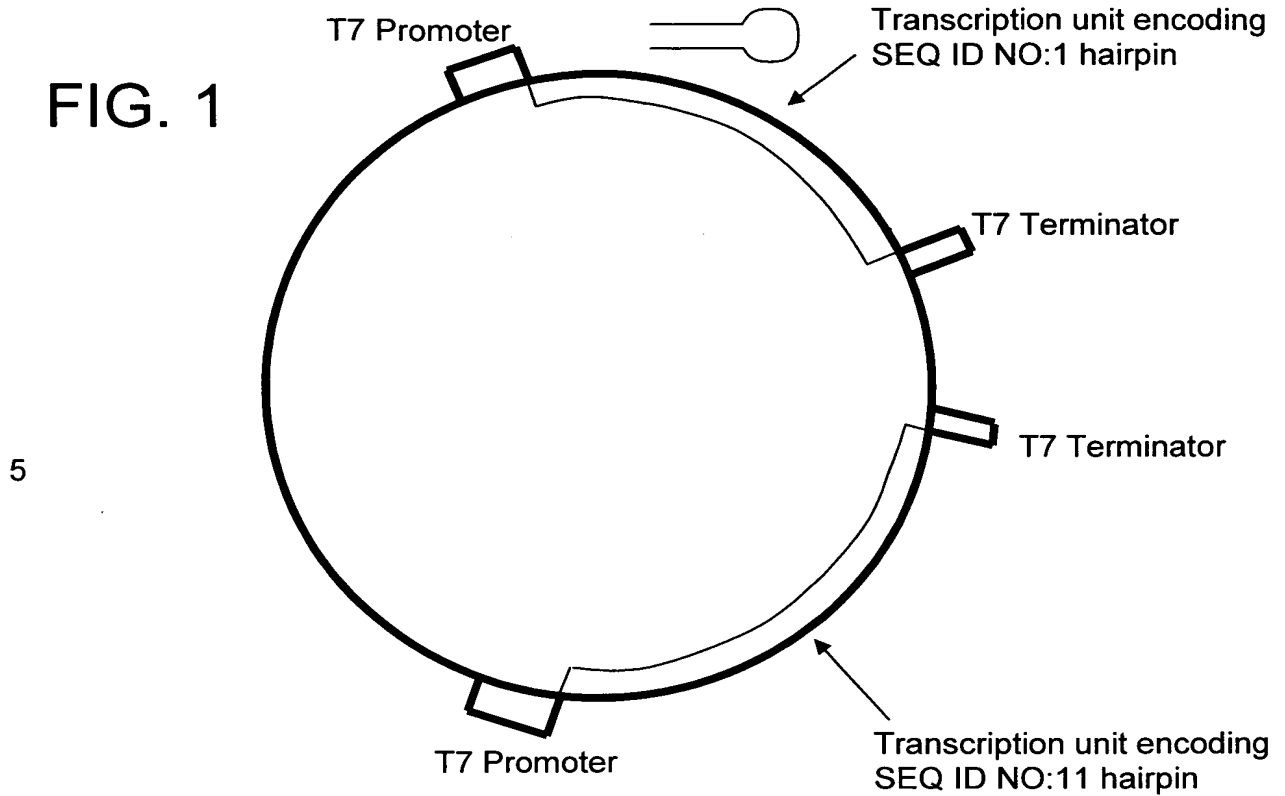


FIG. 2

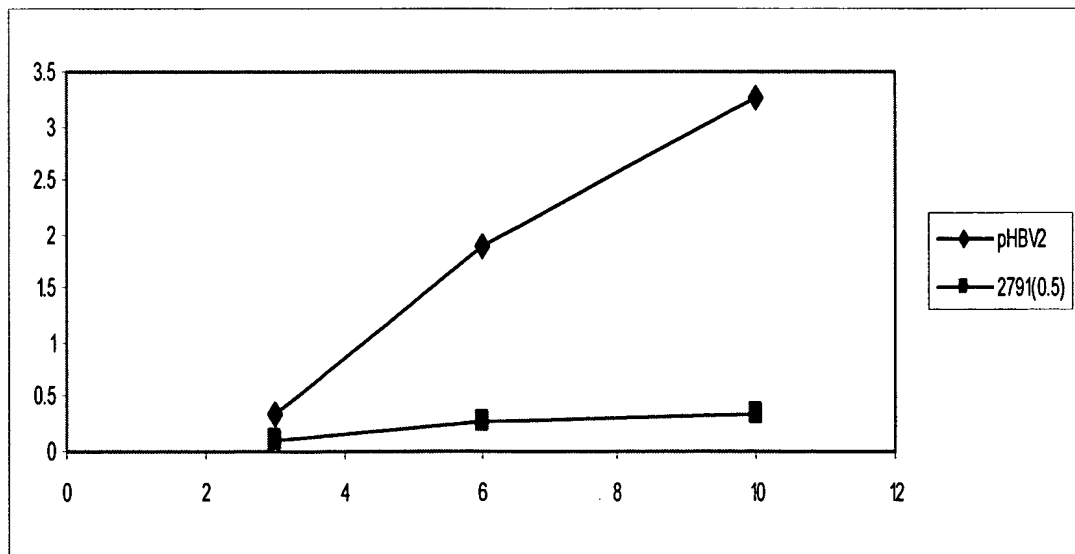


FIG. 3

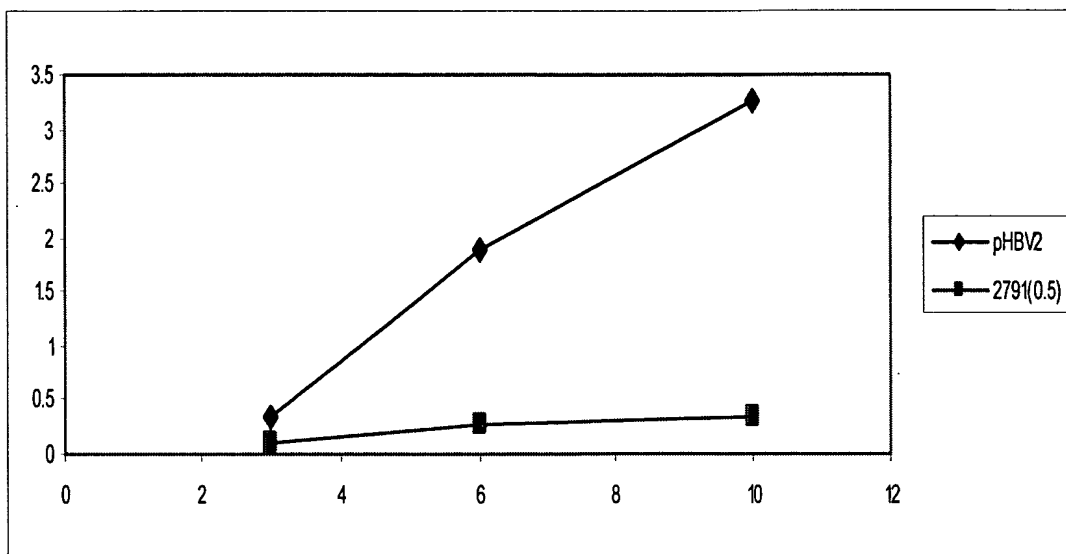


FIG. 4

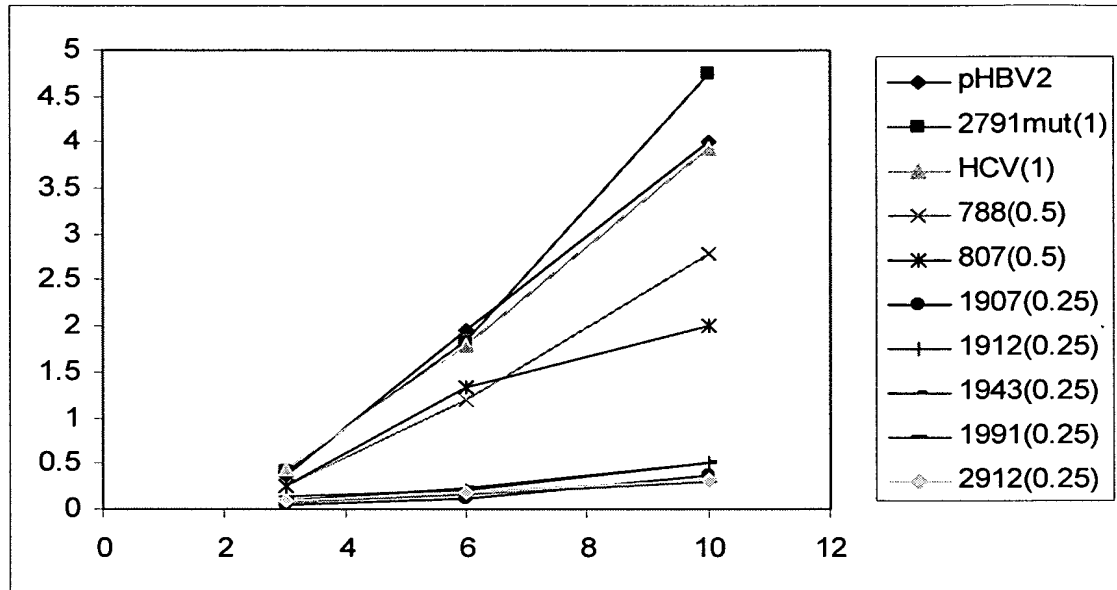


FIG. 5

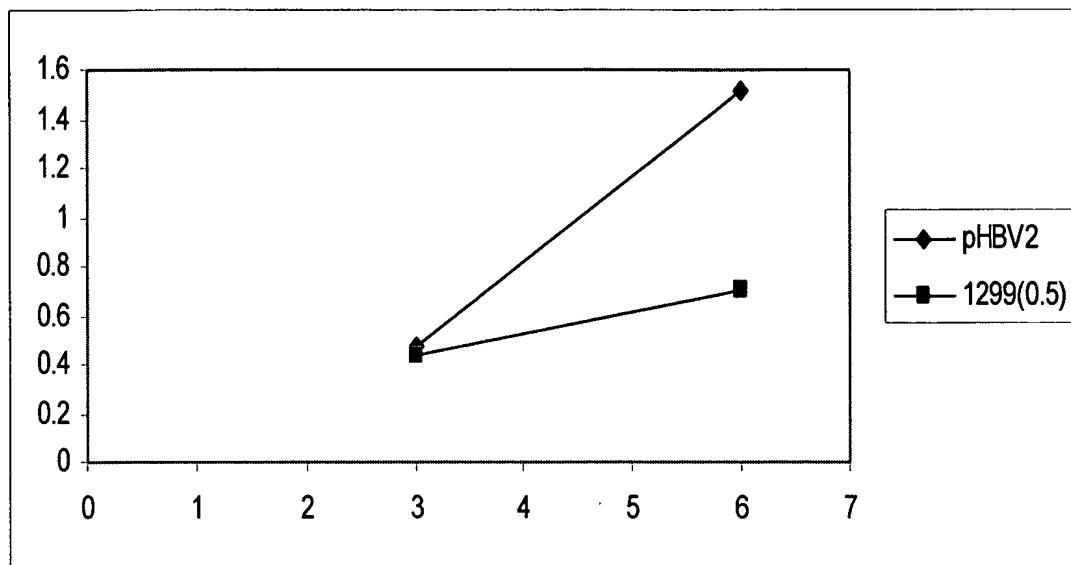


FIG. 6

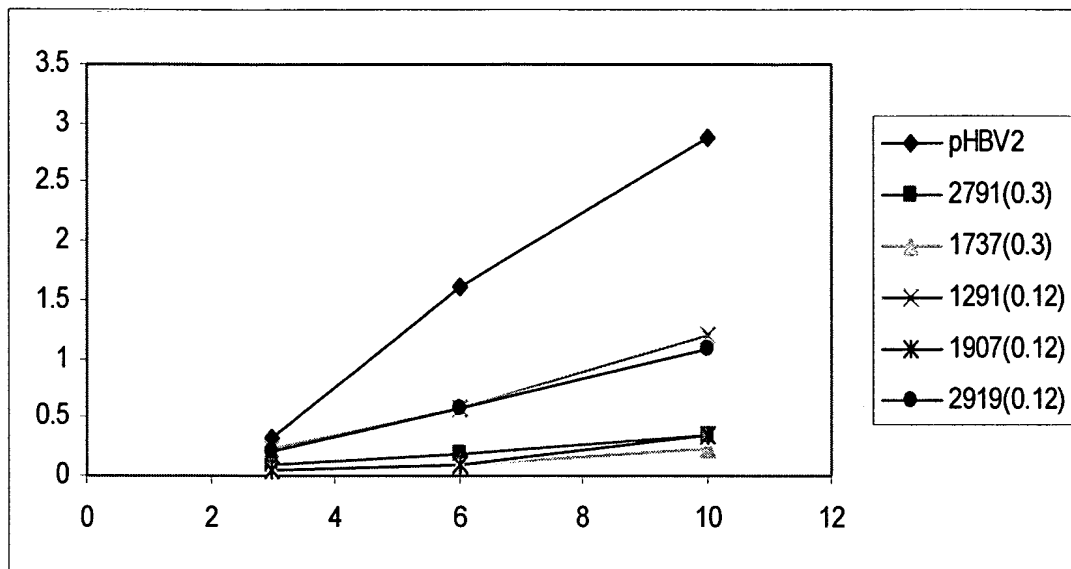


FIG. 7

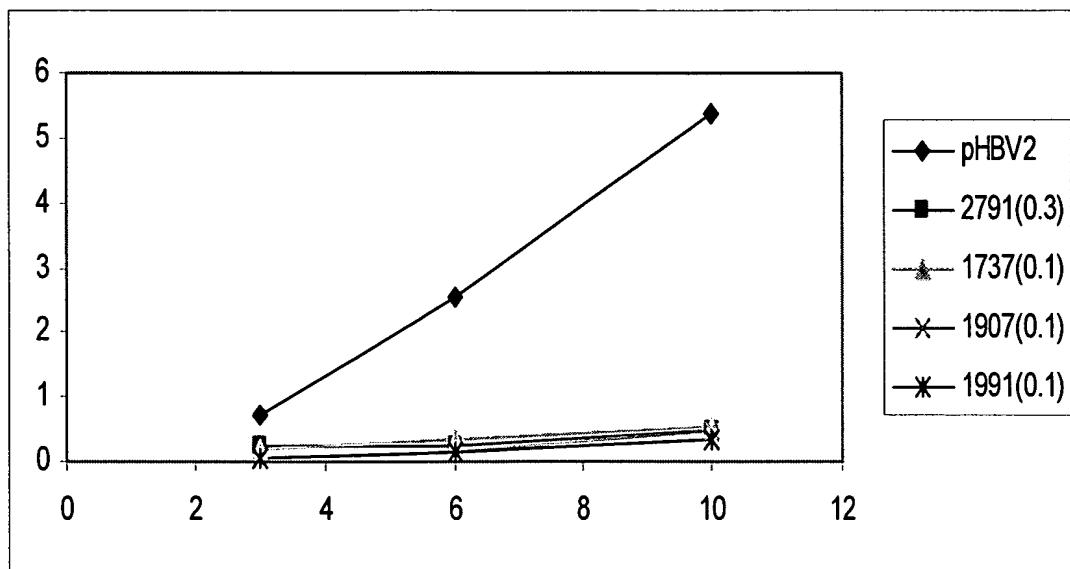
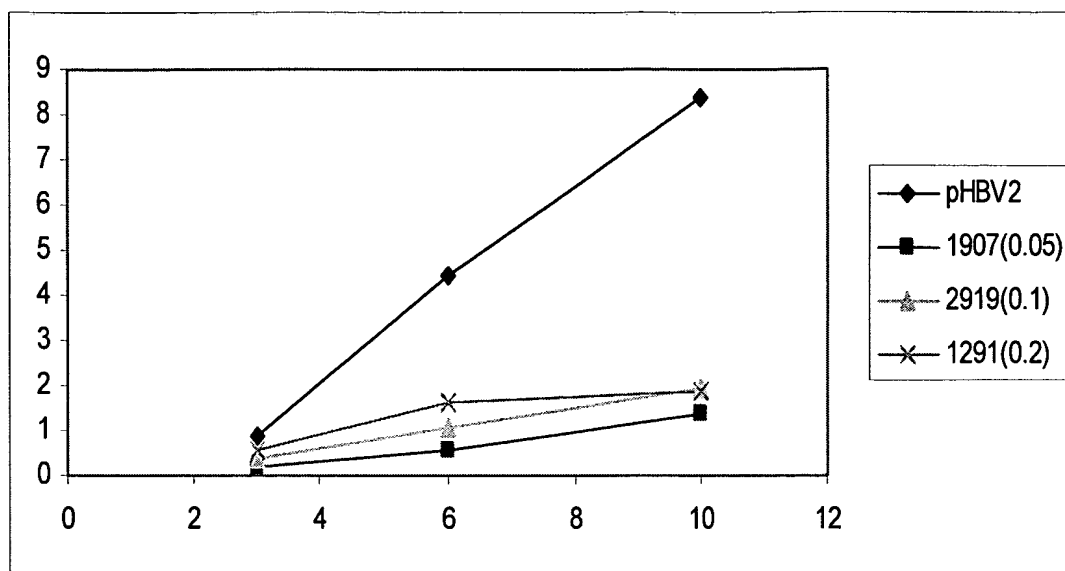


FIG. 8



## FIG. 9

### EFFECTIVE HBV-AYW shRNA INSERTS

5' – GGTCGAC – sense stem – loop – antisense stem – TT – 3'

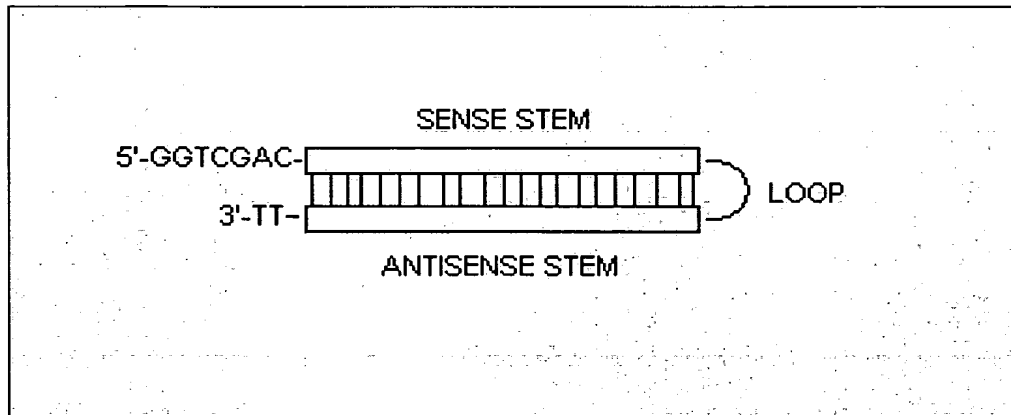




FIG. 10

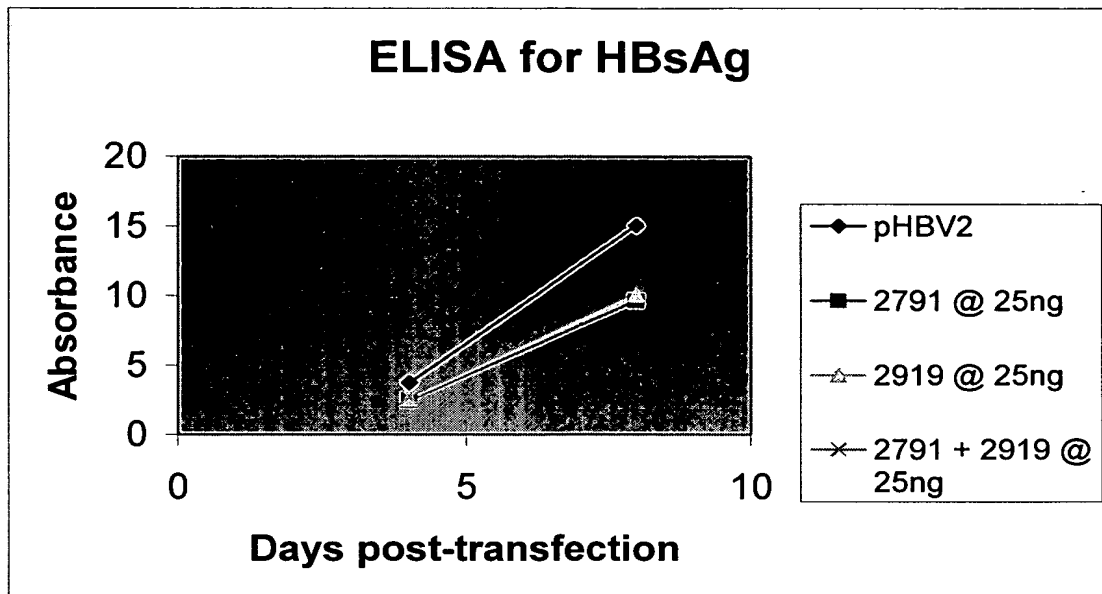


FIG. 11

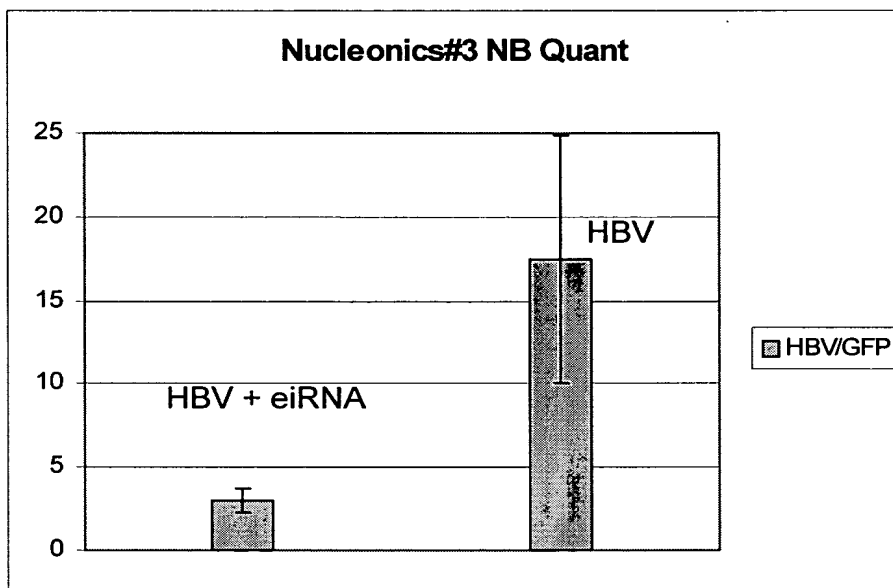


FIG. 12

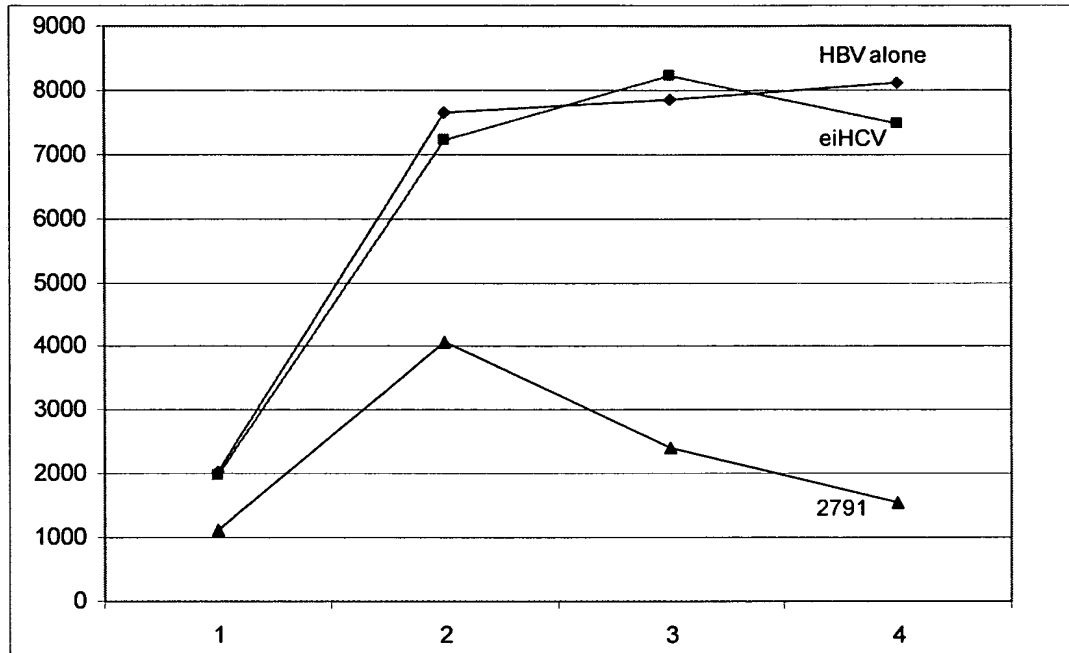


FIG. 13

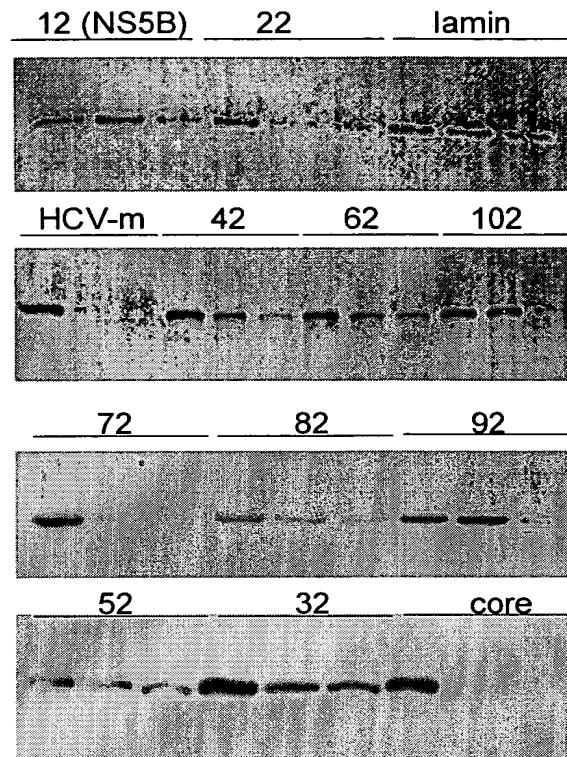
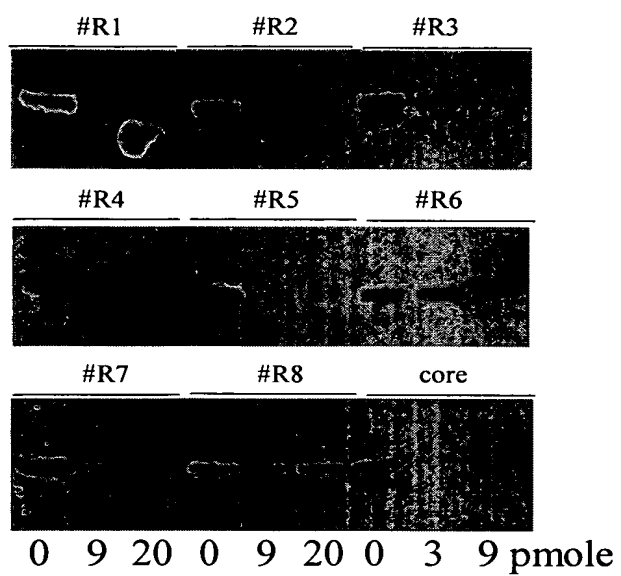


FIG. 14

5



Position	sequence	length
9510-9531	TGGCTCCATCTTAGCCCTAGTC	22
9510-9533	TGGCTCCATCTTAGCCCTAGTCAC	24
9510-9534	TGGCTCCATCTTAGCCCTAGTCACG	25
9510-9535	TGGCTCCATCTTAGCCCTAGTCACGG	26
9510-9536	TGGCTCCATCTTAGCCCTAGTCACGGC	27
9514-9534	TCCATCTTAGCCCTAGTCACG	21
9514-9535	TCCATCTTAGCCCTAGTCACGG	22
9514-9536	TCCATCTTAGCCCTAGTCACGGC	23
9514-9539	TCCATCTTAGCCCTAGTCACGGCTAG	26
9514-9540	TCCATCTTAGCCCTAGTCACGGCTAGC	27
9514-9542	TCCATCTTAGCCCTAGTCACGGCTAGCTG	29
9517-9539	ATCTTAGCCCTAGTCACGGCTAG	23
9517-9540	ATCTTAGCCCTAGTCACGGCTAGC	24
9517-9542	ATCTTAGCCCTAGTCACGGCTAGCTG	26
9517-9544	ATCTTAGCCCTAGTCACGGCTAGCTGTG	28
9518-9539	TCTTAGCCCTAGTCACGGCTAG	22
9518-9540	TCTTAGCCCTAGTCACGGCTAGC	23
9518-9542	TCTTAGCCCTAGTCACGGCTAGCTG	25
9518-9544	TCTTAGCCCTAGTCACGGCTAGCTGTG	27
9520-9540	TTAGCCCTAGTCACGGCTAGC	21
9520-9542	TTAGCCCTAGTCACGGCTAGCTG	23
9520-9544	TTAGCCCTAGTCACGGCTAGCTGTG	25
9520-9548	TTAGCCCTAGTCACGGCTAGCTGTGAAAG	29
9521-9542	TAGCCCTAGTCACGGCTAGCTG	22
9521-9544	TAGCCCTAGTCACGGCTAGCTGTG	24
9521-9548	TAGCCCTAGTCACGGCTAGCTGTGAAAG	28
9521-9549	TAGCCCTAGTCACGGCTAGCTGTGAAAGG	29
9522-9542	AGCCCTAGTCACGGCTAGCTG	21
9522-9544	AGCCCTAGTCACGGCTAGCTGTG	23
9522-9548	AGCCCTAGTCACGGCTAGCTGTGAAAG	27
9522-9549	AGCCCTAGTCACGGCTAGCTGTGAAAGG	28
9527-9548	TAGTCACGGCTAGCTGTGAAAG	22
9527-9549	TAGTCACGGCTAGCTGTGAAAGG	23
9527-9551	TAGTCACGGCTAGCTGTGAAAGGTC	25
9527-9552	TAGTCACGGCTAGCTGTGAAAGGTCC	26
9527-9553	TAGTCACGGCTAGCTGTGAAAGGTCCG	27
9527-9555	TAGTCACGGCTAGCTGTGAAAGGTCCGTG	29
9528-9548	AGTCACGGCTAGCTGTGAAAG	21
9528-9549	AGTCACGGCTAGCTGTGAAAGG	22
9528-9551	AGTCACGGCTAGCTGTGAAAGGTC	24
9528-9552	AGTCACGGCTAGCTGTGAAAGGTCC	25
9528-9553	AGTCACGGCTAGCTGTGAAAGGTCCG	26
9528-9555	AGTCACGGCTAGCTGTGAAAGGTCCGTG	28
9530-9551	TCACGGCTAGCTGTGAAAGGTC	22
9530-9552	TCACGGCTAGCTGTGAAAGGTCC	23
9530-9553	TCACGGCTAGCTGTGAAAGGTCCG	24
9530-9555	TCACGGCTAGCTGTGAAAGGTCCGTG	26
9530-9557	TCACGGCTAGCTGTGAAAGGTCCGTGAG	28
9530-9558	TCACGGCTAGCTGTGAAAGGTCCGTGAGC	29
9532-9552	ACGGCTAGCTGTGAAAGGTCC	21
9532-9553	ACGGCTAGCTGTGAAAGGTCCG	22
9532-9555	ACGGCTAGCTGTGAAAGGTCCGTG	24
9532-9557	ACGGCTAGCTGTGAAAGGTCCGTGAG	26
9532-9558	ACGGCTAGCTGTGAAAGGTCCGTGAGC	27
9532-9559	ACGGCTAGCTGTGAAAGGTCCGTGAGCC	28
9532-9560	ACGGCTAGCTGTGAAAGGTCCGTGAGCCG	29
9537-9557	TAGCTGTGAAAGGTCCGTGAG	21
9537-9558	TAGCTGTGAAAGGTCCGTGAGC	22
9537-9559	TAGCTGTGAAAGGTCCGTGAGCC	23

FIG. 15

9537-9560	TAGCTGTGAAAGGTCCGTGAGCCG	24
9537-9561	TAGCTGTGAAAGGTCCGTGAGCCGC	25
9537-9564	TAGCTGTGAAAGGTCCGTGAGCCGCTTG	28
9538-9558	AGCTGTGAAAGGTCCGTGAGC	21
9538-9559	AGCTGTGAAAGGTCCGTGAGCC	22
9538-9560	AGCTGTGAAAGGTCCGTGAGCCG	23
9538-9561	AGCTGTGAAAGGTCCGTGAGCCGC	24
9538-9564	AGCTGTGAAAGGTCCGTGAGCCGCTTG	27
9538-9566	AGCTGTGAAAGGTCCGTGAGCCGCTTGAC	29
9541-9561	TGTGAAAGGTCCGTGAGCCGC	21
9541-9564	TGTGAAAGGTCCGTGAGCCGCTTG	24
9541-9566	TGTGAAAGGTCCGTGAGCCGCTTGAC	26
9541-9568	TGTGAAAGGTCCGTGAGCCGCTTGACTG	28
9541-9569	TGTGAAAGGTCCGTGAGCCGCTTGACTGC	29
9543-9564	TGAAAGGTCCGTGAGCCGCTTG	22
9543-9566	TGAAAGGTCCGTGAGCCGCTTGAC	24
9543-9568	TGAAAGGTCCGTGAGCCGCTTGACTG	26
9543-9569	TGAAAGGTCCGTGAGCCGCTTGACTGC	27
9543-9571	TGAAAGGTCCGTGAGCCGCTTGACTGCAG	29
9545-9566	AAAGGTCCGTGAGCCGCTTGAC	22
9545-9568	AAAGGTCCGTGAGCCGCTTGACTG	24
9545-9569	AAAGGTCCGTGAGCCGCTTGACTGC	25
9545-9571	AAAGGTCCGTGAGCCGCTTGACTGCAG	27
9545-9573	AAAGGTCCGTGAGCCGCTTGACTGCAGAG	29
9546-9564	AAGGTCCGTGAGCCGCTTGAC	21
9546-9566	AAGGTCCGTGAGCCGCTTGACTG	23
9546-9569	AAGGTCCGTGAGCCGCTTGACTGC	24
9546-9571	AAGGTCCGTGAGCCGCTTGACTGCAG	26
9546-9573	AAGGTCCGTGAGCCGCTTGACTGCAGAG	28
9547-9568	AGGTCCGTGAGCCGCTTGACTG	22
9547-9569	AGGTCCGTGAGCCGCTTGACTGC	23
9547-9571	AGGTCCGTGAGCCGCTTGACTGCAG	25
9547-9573	AGGTCCGTGAGCCGCTTGACTGCAGAG	27
9547-9575	AGGTCCGTGAGCCGCTTGACTGCAGAGAG	29
9550-9571	TCCGTGAGCCGCTTGACTGCAG	22
9550-9573	TCCGTGAGCCGCTTGACTGCAGAG	24
9550-9575	TCCGTGAGCCGCTTGACTGCAGAGAG	26
9550-9577	TCCGTGAGCCGCTTGACTGCAGAGAGTG	28
9550-9578	TCCGTGAGCCGCTTGACTGCAGAGAGTGC	29
9554-9575	TGAGCCGCTTGACTGCAGAGAG	22
9554-9577	TGAGCCGCTTGACTGCAGAGAGTG	24
9554-9578	TGAGCCGCTTGACTGCAGAGAGTGC	25
9554-9580	TGAGCCGCTTGACTGCAGAGAGTGCTG	27
9556-9577	AGCCGCTTGACTGCAGAGAGTG	22
9556-9578	AGCCGCTTGACTGCAGAGAGTGC	23
9556-9580	AGCCGCTTGACTGCAGAGAGTGCTG	25
9556-9584	AGCCGCTTGACTGCAGAGAGTGCTGATAC	29
9562-9584	TTGACTGCAGAGAGTGCTGATAC	23
9562-9586	TTGACTGCAGAGAGTGCTGATACTG	25
9562-9587	TTGACTGCAGAGAGTGCTGATACTGG	26
9562-9588	TTGACTGCAGAGAGTGCTGATACTGGC	27
9562-9589	TTGACTGCAGAGAGTGCTGATACTGGCC	28
9563-9584	TGACTGCAGAGAGTGCTGATAC	22
9563-9586	TGACTGCAGAGAGTGCTGATACTG	24
9563-9587	TGACTGCAGAGAGTGCTGATACTGG	25
9563-9588	TGACTGCAGAGAGTGCTGATACTGGC	26
9563-9589	TGACTGCAGAGAGTGCTGATACTGGCC	27
9563-9591	TGACTGCAGAGAGTGCTGATACTGGCCTC	29
9565-9586	ACTGCAGAGAGTGCTGATACTG	22
9565-9587	ACTGCAGAGAGTGCTGATACTGG	23

9565-9588	ACTGCAGAGAGTGCTGATACTGGC	24
9565-9589	ACTGCAGAGAGTGCTGATACTGGCC	25
9565-9591	ACTGCAGAGAGTGCTGATACTGGCCTC	27
9565-9593	ACTGCAGAGAGTGCTGATACTGGCCTCTC	29
9567-9587	TGCAGAGAGTGCTGATACTGG	21
9567-9588	TGCAGAGAGTGCTGATACTGGC	22
9567-9589	TGCAGAGAGTGCTGATACTGGCC	23
9567-9591	TGCAGAGAGTGCTGATACTGGCCTC	25
9567-9593	TGCAGAGAGTGCTGATACTGGCCTCTC	27
9567-9595	TGCAGAGAGTGCTGATACTGGCCTCTCTG	29
9570-9591	AGAGAGTGCTGATACTGGCCTC	22
9570-9593	AGAGAGTGCTGATACTGGCCTCTC	24
9570-9595	AGAGAGTGCTGATACTGGCCTCTCTG	26
9570-9596	AGAGAGTGCTGATACTGGCCTCTCTGC	27
9570-9598	AGAGAGTGCTGATACTGGCCTCTCTGCAG	29
9572-9593	AGAGTGCTGATACTGGCCTCTC	22
9572-9595	AGAGTGCTGATACTGGCCTCTCTG	24
9572-9596	AGAGTGCTGATACTGGCCTCTCTGC	25
9572-9598	AGAGTGCTGATACTGGCCTCTCTGCAG	27
9574-9595	AGTGCTGATACTGGCCTCTCTG	22
9574-9596	AGTGCTGATACTGGCCTCTCTGC	23
9574-9598	AGTGCTGATACTGGCCTCTCTGCAG	25
9574-9601	AGTGCTGATACTGGCCTCTCTGCAGATC	28
9576-9596	TGCTGATACTGGCCTCTCTGC	21
9576-9598	TGCTGATACTGGCCTCTCTGCAG	23
9576-9601	TGCTGATACTGGCCTCTCTGCAGATC	26
9576-9604	TGCTGATACTGGCCTCTCTGCAGATCAAG	29
9579-9601	TGATACTGGCCTCTCTGCAGATC	23
9579-9604	TGATACTGGCCTCTCTGCAGATCAAG	26
9581-9601	ATACTGGCCTCTCTGCAGATC	21
9581-9604	ATACTGGCCTCTCTGCAGATCAAG	24
9583-9604	ACTGGCCTCTCTGCAGATCAAG	22



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